

1/32

FIG. 1A

Input file Fbh56919FL2.seq
Sequence length 3003

TTCGGCACAGGCTGCTGCGGGGAGCTCTTTCTGAGGTACTGTGGAGCACCCAAAGTCTGTGAGCCCTCTGGCCGTGC

AAACAGGCCACAGAGGAAACAGACCTTGCTTATTACCCACAGCCCTGGGACGTCTCTTCTCCAGAGTCTCCATCAGCTT

TGCTAATCGACTGATTGGAAATAATTCCTCAACACACCAAGTCAAGGATACAGGACGAGCGGCTCCCTGTTGTAT

GGACATTCTGCACCCGAACTAGCTGAGTCTCCTGAAGTTTATGTTATGAACAGAGAACTTTCATCCAGCACAT

M D E S A L T L G T I D V
GATTTGGGAATACACTTTGTGAC ATG GAT GAA TCT GCA CTG ACC CTT GGT ACA ATA GAT GTT 13 39

S Y L P H S S E Y S V G R C K H T S E E
TCT TAT CTG CCA CAT TCA TCA GAA TAC AGT GTT GGT CGA TGT AAG CAC ACA AGT GAG GAA 33 99

W G E C G F R P T V F R S A T L K W K E
TGG GGT GAG TGT GGC TTT AGA CCC ACC GTC TTC AGA TCT GCA ACT TTA AAA TGG AAA GAA 53 159

S L M S R K R P F V G R C C Y S C T P Q
AGC CTA ATG AGT CGG AAA AGG CCA TTT GTT GGA AGA TGT TAC TCC TGC ACT CCC CAG 73 219

S W D K F F N P S I P S L G L R N V I Y
AGC TGG GAC AAA TTT TTC AAC CCC AGT ATC CCG TCT TTG GGT TTG CGG AAT GTT ATT TAT 93 279

I N E T H T R R H R G W L A R R L S Y V L
ATC AAT GAA ACT CAC ACA AGA CAC CGC GGA TGG CTT GCA AGA CGC CTT TCT TAC GTT CTT 113 339

F I Q E R D V H K G M F A T N V T E N V
TTT ATT CAA GAG CGA GAT GTG CAT AAG GGC ATG TTT GCC ACC AAT GTG ACT GAA AAT GTG 133 399

2/32

FIG. 1B

153 L N S S R V Q E A I A E V A A E L N P D
 459 CTG AAC AGC AGT AGA GTA CAA GAG GCA ATT GCA GAA GTG GCT GCT GAA TTA AAC CCT GAT
 173 G S A Q Q Q S K A V N K V K K A K R I
 519 GGT TCT GCC CAG CAG CAA TCA AAA GCC GTT AAC AAA GTG AAA AAG AAA GCT AAA AGG ATT
 193 L Q E M V A T V S P A M I R L T G W V L
 579 CTT CAA GAA ATG ATG GCT GCC ACT GTC TCA CCG GCA ATG ATC AGA CTG ACT GGG TGG GTG CTG
 213 L K L F N S F F W N I Q I H K G Q L E M
 639 CTA AAA CTG TTC AAC AGC TTC TTT TGG AAC ATT CAA ATT CAC AAA GGT CAA CTT GAG ATG
 233 V K A A T E T N L P L L F L P V H R S H
 699 GTT AAA GCT GCA ACT GAG ACG AAT TTG CCG CTT CTG TTT CTA CCA GTT CAT AGA TCC CAT
 253 I D Y L L L T F I L F C H N I K A P Y I
 759 ATT GAC TAT CTG CTG CTC ACT TTC ATT CTC TTC TGC CAT AAC ATC AAA GCA CCA TAC ATT
 273 A S G N N L N I P Y F S T L I H K L G G
 819 GCT TCA GGC AAT AAT CTC AAC ATC CCA ATC TTC AGT ACC TTG ATC CAT AAG CTT GGG GGC
 293 F F I R K R L D E T P D G R K D V L Y R
 879 TTC TTC ATA CGA AGG CTC GAT GAA ACA CCA GAT GGA CGG AAA GAT GTT CTC TAT AGA
 313 A L L H G H I V E L L R Q Q Q F L E I F
 939 GCT TTG CTC CAT GGG CAT ATA GTT GAA TTA CTT CGA CAG CAG CAA TTC TTG GAG ATC TTC
 333 L E G T R S R S G K T S C A R A G L L S
 999 CTG GAA GGC ACA CGT TCT AGG AGT GGA AAA ACC TCT TGT GCT CGG GCA GGA CTT TTG TCA

3/32

FIG. 1C

V	V	V	D	T	L	S	T	N	V	I	P	D	I	L	I	I	P	V	G	353
GTT	GTG	GTA	GAT	ACT	CTG	TCT	ACC	AAT	GTC	ATC	CCA	GAC	ATC	TTG	ATA	ATA	CCT	GTT	GGA	1059
I	S	Y	D	R	I	I	E	G	H	Y	N	G	E	Q	L	G	K	P	K	373
ATC	TCC	TAT	GAT	CGC	ATT	ATC	GAA	GGT	CAC	TAC	AAT	GGT	GAA	CAA	CTG	GGC	AAA	CCT	AAG	1119
K	N	E	S	L	W	S	V	A	R	G	V	I	R	M	L	R	K	N	Y	393
AAG	AAT	GAG	AGC	CTG	TGG	AGT	GTA	GCA	AGA	GGT	GTT	ATT	AGA	ATG	TTA	CGA	AAA	AAC	TAT	1179
G	C	V	R	V	D	F	A	Q	P	F	S	L	K	E	Y	L	E	S	Q	413
GGT	TGT	GTC	CGA	GTG	GAT	TTT	GCA	CAG	CCA	TTT	TCC	TTA	AAG	GAA	TAT	TTA	GAA	AGC	CAA	1239
S	Q	K	P	V	S	A	L	L	S	L	E	Q	A	L	L	P	A	I	L	433
AGT	CAG	AAA	CCG	GTG	TCT	GCT	CTA	CTT	TCC	CTG	GAG	CAA	GCG	TTG	TTA	CCA	GCT	ATA	CTT	1299
P	S	R	P	S	D	A	A	D	E	G	R	D	T	S	I	N	E	S	R	453
CCT	TCA	AGA	CCC	AGT	GAT	GCT	GCT	GAT	GAA	GGT	AGA	GAC	ACG	TCC	ATT	AAT	GAG	TCC	AGA	1359
N	A	T	D	E	S	L	R	R	L	I	A	N	L	A	E	H	I	L	L	473
AAT	GCA	ACA	GAT	GAA	TCC	CTA	CGA	AGG	AGG	TTG	ATT	GCA	AAT	CTG	GCT	GAG	CAT	ATT	CTA	1419
F	T	A	S	K	S	C	A	I	M	S	T	H	I	V	A	C	L	L	L	493
TTC	ACT	GCT	AGC	AAG	TCC	TGT	GCC	ATT	ATG	TCC	ACA	CAC	ATT	GTG	GCT	TGC	CTG	CTC	CTC	1479
Y	R	H	R	Q	G	I	D	L	S	T	L	V	E	D	F	F	V	M	K	513
TAC	AGA	CAC	AGG	CAG	GGA	ATT	GAT	CTC	TCC	ACA	TTG	GTC	GAA	GAC	TTT	TTT	GTG	ATG	AAA	1539
E	E	V	L	A	R	D	F	D	L	G	F	S	G	N	S	E	D	V	V	533
GAG	GAA	GTC	GCT	GCT	GAT	TTT	GAC	CTG	GGG	TTC	TCA	GGA	AAT	TCA	GAA	GAT	GTA	GTA	GTA	1599

FIG. 1D

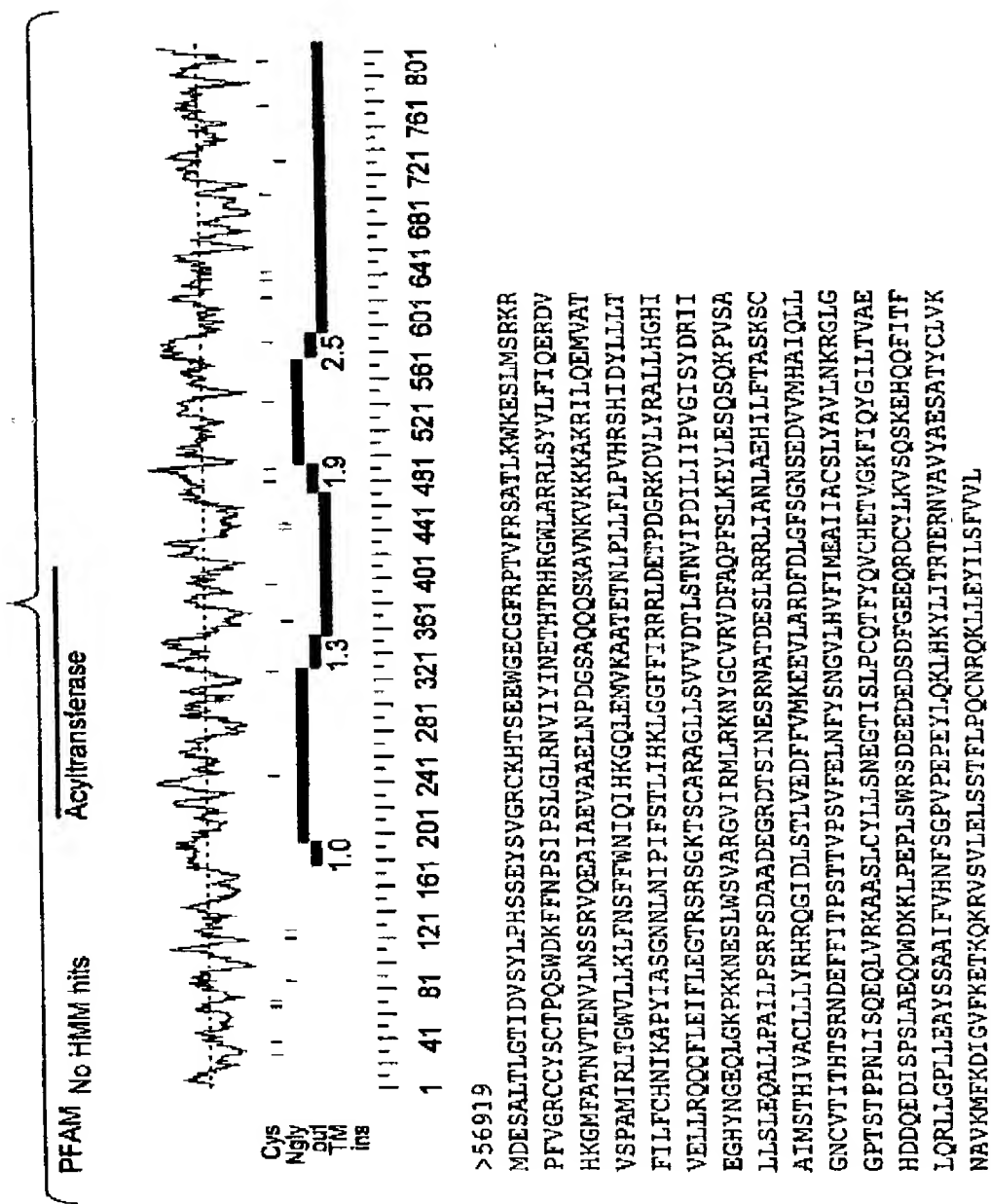
M	H	A	I	Q	L	L	G	N	C	V	T	I	T	H	T	S	R	N	D	553
ATG	CAT	GCC	ATA	CAG	CTG	CTG	GGG	AAT	TGT	GTC	ACA	ATC	ACC	CAC	ACT	AGC	AGG	AAC	GAT	1659
E	F	F	I	T	P	S	T	T	V	P	S	V	F	E	L	N	F	Y	S	573
GAG	TTT	TTT	ATC	ACC	CCC	AGC	ACA	ACT	GTC	CCA	TCA	GTC	TTC	GAA	CTC	AAC	TTC	TAC	AGC	1719
N	G	V	L	H	V	F	I	M	E	A	I	I	A	C	S	L	Y	A	V	593
AAT	GGG	GTA	CTT	CAT	GTC	TTT	ATC	ATG	GAG	GCC	ATC	ATA	GCT	TGC	AGC	CTT	TAT	GCA	GTT	1779
L	N	K	R	G	L	G	G	P	T	S	T	P	P	N	L	I	S	Q	E	613
CTG	AAC	AAG	AGG	GGA	CTG	GGG	GGT	CCC	ACT	AGC	ACC	CCA	CCT	AAC	CTG	ATC	AGC	CAG	GAG	1839
Q	L	V	R	K	A	A	S	L	C	Y	L	L	S	N	E	G	T	I	S	533
CAG	CTG	GTG	CGG	AAG	GCG	GCC	AGC	CTG	TGC	TAC	CTT	CTC	TCC	AAT	GAA	GGC	ACC	ATC	TCA	1899
L	P	C	Q	T	F	Y	Q	V	C	H	E	T	V	G	K	F	I	Q	Y	553
CTG	CCT	TGC	CAG	ACA	TTT	TAC	CAA	GTC	TGC	CAT	GAA	ACA	GTA	GGA	AAG	TTT	ATC	CAG	TAT	1959
G	I	L	T	V	A	E	H	D	D	Q	E	D	I	S	P	S	L	A	E	673
GGC	ATT	CTT	ACA	GTG	GCA	GAG	CAC	GAT	GAC	CAG	GAA	GAT	ATC	AGT	CCT	AGT	CTT	GCT	GAG	2019
Q	Q	W	D	K	K	L	P	E	P	L	S	W	R	S	D	E	E	D	E	693
CAG	CAG	TGG	GAC	AAG	AAG	CTT	CCA	GAA	CCT	TTG	TCT	TGG	AGA	AGT	GAT	GAA	GAA	GAT	GAA	2079
D	S	D	F	G	E	E	Q	R	D	C	Y	L	F	V	S	Q	S	K	E	713
GAC	AGT	GAC	TTT	GGG	GAG	GAA	CAG	CGA	GAT	TGC	TAC	CTG	AAG	GTG	AGC	CAA	TCC	AAG	GAG	2139
H	Q	Q	F	I	T	F	L	Q	R	L	L	G	P	L	L	E	A	Y	S	733
CAC	CAG	CAG	TTT	ATC	ACC	TTC	TTA	CAG	AGA	CTC	CTT	GGG	CCT	TTG	CTG	GAG	GCC	TAC	AGC	2199

11
12
13

GTAA CGTGTGGCACTGCTGGCAATGAAGGTCATGAGATGAGTTCCTTGTAGGTACCAAGCTTCTGGCTCAAGAGTTTGA
AGGTGCCCTTCCAGGGGTCAAGCCCTGCTGTTNCCGAAGTGAATCTCTGGAAGCAAGTGCCCTTCTNCTCCATGCAATC
TGAGATCTTCCAGCTTT

6/32

FIG. 2



7/32

FIG. 3A

Protein Family / Domain Matches, HMMer version 2

Searching for complete domains in PFAM
 hmmpfam - search a single seq against HMM database
 HMMER 2.1.1 (Dec 1998)
 Copyright (C) 1992-1998 Washington University School of Medicine
 HMMER is freely distributed under the GNU General Public License (GPL).

 HMM file: /prod/ddm/seqanal/pfam6.4/Pfam
 Sequence file: /prod/ddm/wspace/orfanal/oa-script.21255.seq

Query: 56919

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
Acyltransferase	Acyltransferase	126.1	6.4e-34	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
Acyltransferase	1/1	215	412 ..	1	195 {}	126.1	6.4e-34

8/32

FIG. 3B

Alignments of top-scoring domains:

Acyltransferase: domain 1 of 1, from 215 to 412: score 126.1, E = 6.4e-34

*->lenlpkkgaivvsNHRsYdIlvlsaalprigpwlrvrlvfiakke

+ +++++ p ++ + HRS+D41+1 ++l++++ ++ +ia ++

56919 215 KAATETNLPFLFVHRSHIDYLLLTFFILFCHN-----IKAPYIASGN 257

llkvPlIfGwlmrlagafidRmra.....kdalaaadelvrvlellrx

+l++P+ f++l+ ++g +fi+R+ ++++++kd l++a+ + + tellr+

56919 258 NINIPi-FSTLIHKLGGFFIRRLDEtpdgrKDVLYRALLGHIVELLRQ 306

grsvliFPEGTRrsrgellppfKkGia.....afrlAlkagvpivPvviv

+ + iF EGTRsrsg++ + ++G++ + + ++ ++ i+Pv+i

56919 307 QQFLElFLEGTRSRSGKTSC-ARAGLLsvvvdTLSTNVIPDILIIIPVGI- 354

sgreelepknegkllrlarkkgpvtvrvlppipld..pedikelaelr

s++ ++e ++++ + ++++++ v +++ +++++ +

56919 355 SYDRlIEGHYNCEQ--LGKPKNESlMSVARGVIRMIRKNYSCVRVDFAQ 402

dilvqaleel<*

+ +++++ e+

56919 403 PPSLKEYLES 412

9/32

FIG. 4A

ProDom Matches ProDomId	Start	End	Description	Score
View Prodom PD347660	1	55	p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION MITOCHONDRIAL	250
View Prodom PD087501	51	158	p2001.1 (1) // AIP2-DLD1	77
View Prodom PD353751	56	152	p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION MITOCHONDRIAL	500
View Prodom PD037846	128	259	p2001.1 (15) PLSB(5) DAPT(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE PHOSPHOLIPID GPAT BIOSYNTHESIS MITOCHONDRIAL TRANSMEMBRANE PRECURSOR MITOCHONDRION	258
View Prodom PD042466	259	590	p2001.1 (16) PLSB(4) DAPT(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE BIOSYNTHESIS PHOSPHOLIPID GPAT PRECURSOR MITOCHONDRIAL TRANSMEMBRANE MITOCHONDRION	413
View Prodom PD025192	462	649	p2001.1 (4) PLSB(3) // ACYLTRANSFERASE PHOSPHOLIPID MITOCHONDRIAL BIOSYNTHESIS PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION	

10/32

FIG. 4B

458

View Prodom PD042027 465 673 p2001.1 (6) PLSB(2) // ACYLTRANSFERASE
GLYCEROL-3-PHOSPHATE MEMBRANE
PHOSPHOLIPID GPAT BIOSYNTHESIS MUTANT

80

View Prodom PD042760 650 828 p2001.1 (2) PLSB(2) // ACYLTRANSFERASE
PHOSPHOLIPID BIOSYNTHESIS PRECURSOR
TRANSMEMBRANE GLYCEROL-3-PHOSPHATE
GPAT MITOCHONDRION MITOCHONDRIAL

799

View Prodom PD042760

>PD042760 p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS
PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION
MITOCHONDRIAL

Length = 179

Score = 799 (286.3 bits), Expect = 1.2e-79, P = 1.2e-79
Identities = 155/179 (86%), Positives = 161/179 (89%)

Query: 650 FIQYGILTVAEHDDQEDISPSLAQQQWDKKLPEPLSWRXXXXXXXXXXXXXQORDCYLKVS 709

FIQYGILTVAE DDQED+SP LAEQQW+KKLPEPL+WR QORDCYLKVS

Sbjct: 1 FIQYGILTVAEQDDQEDVSPGLAEQQWKKLPEPLNWRSDDEDESDDFGEEQORDCYLKVS 60

Query: 710 QSKEHQQFITFLQRLGLPLLEAYSSAAIFVHNFGVPPEPEYLQKLHKYLIITRERNVAV 769

Q+KEHQQFITFLQRLGLPLLEAYSSAAIFVHNF GPVPE EYLQKLH+YLIITRERNVAV

Sbjct: 61 QAKEHQQFITFLQRLGLPLLEAYSSAAIFVHNFRGPVPESEYLQKLHRYLIITRERNVAV 120

Query: 770 YAESATYCLVKNVAKMFKDIGVFKETKQKRVSVLELSSTFLPQCNQKLLLEYILSFVVL 828

YAESATYCLVKNVAKMFKDIGVFKETKQKRV SVLELS+TFLPQCNQKLLLEYILSFVVL

Sbjct: 121 YAESATYCLVKNVAKMFKDIGVFKETKQKRVSVLELSSTFLPQCNQKLLLEYILSFVVL 179

09035240.030402

11/32

FIG. 4C

View Prodom PD353751

>PD353751 p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS
 PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION
 MITOCHONDRION

Length = 97

Score = 500 (181.1 bits), Expect = 2.1e-47, P = 2.1e-47
 Identities = 90/97 (92%), Positives = 97/97 (100%)

Query: 56 MSKRPFVGRCCYCTPQSWDKFFNPSPISGLRNVIYINETHTRHGWLARRLSYVLF 115
 MSKRPFVGRCCYCTPQSW++FFNPSPISGLRNVIYINETHTRHGWLARRLSY+LF+
 Sbjct: 1 MSKRPFVGRCCYCTPQSWERFFNPSPISGLRNVIYINETHTRHGWLARRLSYILFV 60

Query: 116 QERDVHKGMFATNVNENLNSSRVQEAIAEVAELNP 152
 QERDVHKGMFAT++T+NVLNSSRVQEAIAEVAELNP
 Sbjct: 61 QERDVHKGMFATSITDNVLNSSRVQEAIAEVAELNP 97

View Prodom PD025192

>PD025192 p2001.1 (4) PLSB(3) // ACYLTRANSFERASE PHOSPHOLIPID MITOCHONDRION
 BIOSYNTHESIS PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT
 MITOCHONDRION

Length = 194

Score = 458 (166.3 bits), Expect = 8.7e-43, P = 8.7e-43
 Identities = 95/192 (49%), Positives = 126/192 (65%)

Query: 462 RRLIANLAEHILFTASKSCAISMTHIVACLLYRHRQIDLSITLVEDFFVMKEEVLARDF 521
 R LI ++ EH++F S C+INSTH+VACLLL R R G+ STL ED + E++IA
 Sbjct: 3 RNLIRSIGEHVVFDCSMNCSSINSTHVACLLITWRNGVHRSTLEEDCDNLCEKILAEFG 62

12/32

FIG. 4D

Query: 522 DL-GFSGNS---EDVVMHAIQLGNCVTITHTSRNDEFFITPSTTVPSVFELNFSNGVL 577
 D+ GFSG S +V +A +LLG+CVT+T RNDEF+I+P +VPS EL +YSN V+
 Sbjct: 63 DIVGFSGKSTKGSQIVKYACELLGSCVTVTDEDRNDEFYISPKNSVPSFIELAYVNSVI 122

Query: 578 HVFIMEAIIACSLYAVLNKRGGLGPTSTPPNLISQELVRKAASLCYLLSNEGTSILPCQ 637
 F +++IIAC++Y++ NK GG NLISQELV A SIC L E PCQ
 Sbjct: 123 CHFALKSIIACTIYSLPNKTKNGGEAGLGNLISQELVEDALSICDMLQVEFMFCRPCQ 182

Query: 638 TFYQVCHETVGK 649
 T ++CH T+GK
 Sbjct: 183 TLRELCHNTLGK 194

View Prodom PD042466

>PD042466 p2001.1 (16) PLSB(4) DAPT(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE
 BIOSYNTHESIS PHOSPHOLIPID GPAT PRECURSOR MITOCHONDRIAL TRANSMEMBRANE
 MITOCHONDRION
 Length = 299

Score = 413 (150.4 bits), Expect = 4.7e-42, Sum P(2) = 4.7e-42
 Identities = 79/152 (51%), Positives = 108/152 (71%)

Query: 259 LNIFPFTLIHKLGGFFIRRLDETPDGRKDVLYRALLHGHIVELLRQQQFLEIFLEGTR 318
 L++PI +L+ + G FFIRR D TP+G+ D LYRA+ H ++ +L+ + +E F+EGTR
 Sbjct: 2 LSMPTMGSLLRRTGAFFIRRSFDPPTPEGKGDQLYRAVFHEVYAQLISKGYNIEFFIEGTR 61

Query: 319 SRSKTSICARAGLLSVVVDTLSTNVIPDILIIIPVGISYDRIIEGH-YNCEQLGKPKKNES 377
 SR+GK + GLLS+VV+ +PDIL++PV ISYDRIIEG+ Y E G PKK ES
 Sbjct: 62 SRTGKNLPKTKGLLSMVVEAFIRGSPVDILLVPVVISYDRIIEGNTYAHELRGAPKKES 121

13/32

FIG. 4E

Query: 378 LMSVARGVIRMLRKNYGVVRVDFQAQPSLKEY 409
 LW + RGV +ML++NYG V VDF +P SL+EY
 Sbjct: 122 LMQFRGVRRMLKRNQGQVYVDFGEPISLREY 153

Score = 64 (27.6 bits), Expect = 4.7e-42, Sum P(2) = 4.7e-42
 Identities = 30/143 (20%), Positives = 59/143 (41%)

Query: 453 RNATDESIRRRLLIANLAEHILFTASKSCAIMSTHIVACLLLYRHRQSIDLSTL---VEDF 509
 RN + + +R + ++ + + ++ + +T +V+ LLL + L L ++D
 Sbjct: 160 RNTYNCAPKRLALQKMSFEVAVRILQATPVTATGLVSALLLTTRGTALTLDQLHHTLQDS 219

Query: 510 FVMKEVLAROFDLGFGNSDVMVHAIQLL--GNCVTITHTSRNDEFFITPSTTVPSVF 567
 E + S + V A L G+ VT + R ++I P + F
 Sbjct: 220 LDYLERKQSPVSTSLRLRSREGVRAADALSNGHPVTRVDSGREPVWYIAPDDEHAAAF 279

Query: 568 ELNPFYNGVLHVFMELIACSL 590
 Y N V+H F+ +I+ +L
 Sbjct: 280 -----YRNSVIHAFLETSIVELAL 298

View Prodom PD037846

>PD037846 p2001.1 (15) PLSB(5) DAPT(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE
 PHOSPHOLIPID GPAT BIOSYNTHESIS MITOCHONDRIAL TRANSMEMBRANE PRECURSOR
 MITOCHONDRION
 Length = 345

Score = 258 (95.9 bits), Expect = 3.4e-21, P = 3.4e-21
 Identities = 56/132 (42%), Positives = 79/132 (59%)

14/32

FIG. 4F

Query: 128 NVTENVLNSSRVQEAIAEVAELNPDGSAQQSQSXXXXXXXXXXXXXRIQEMVATVSPAMIR 187
 N+ +NVLNS + I + A++ S IL EM T++ MIR
 Sbjct: 223 NLKKNVLNSEEIHYVIEQ-----EAKESSTSIDKVRREAREILDEMSHTLNMGNIR 273

Query: 188 LTGWLLKLFNSFWNIQIHKGOLEMVKAATEINLPLFLPVHRSHIDYLLLTFLFCHN 247
 GWL K+FN F I +++ Q+E +K ATE P+++LP HRSHIDYLLL+FIL+ ++
 Sbjct: 274 FCGWVLSKIFNRIFSGICVNEEQIEKIKRATEQGHPIYLPSPHRSHIDYLLLSFILLHYD 333

Query: 248 IKAPYIASGNL 259
 IK P+IA+G NL
 Sbjct: 334 IKVPHIAAGMNL 345

View Prodom PD347660

>PD347660 p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS
 PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION
 MITOCHONDRIAL
 Length = 55

Score = 250 (93.1 bits), Expect = 2.4e-20, E = 2.4e-20
 Identities = 43/55 (78%), Positives = 53/55 (96%)

Query: 1 MDESALTIGTIDVSYLPSPSEYSVGRCKHTSEWGEQGFPTVFRSATLKWKESL 55
 M+ES++T+GTIDVSYLP+SSEYS+GRCKHT+E+W +CGF+PT FRSATLKWKESL
 Sbjct: 1 MEESVITIGTIDVSYLPNSSEYSGLGRCKHTNEDWDVDCGFKPTFRSATLKWKESL 55

15/32

FIG. 4G

View Prodom PD042027

>PD042027 p2001.1 (6) PLSB(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE MEMBRANE
PHOSPHOLIPID GPAT BIOSYNTHESIS MUTANT

Length = 345

Score = 80 (33.2 bits), Expect = 0.11, Sum P(2) = 0.10

Identities = 31/129 (24%), Positives = 60/129 (46%)

Query: 465 IANLAEHILFTASKSCAIMSTHIVACLLLYRHRQGIDLSTLVE--DFFVMKEEVLARDFD 522
+ +LA+ I+ + + A+ ++ A LL ++ + L+E D ++ + D

Sbjct: 32 VNHLAKQIMTHINDAAAVNPMNLCATALLSTRQALGEEQLIEQLDCYLKLLRNVPYSTD 91

Query: 523 LGFSGNS-EDVVMHAIQ--LLGNCVTITHTSRNDEFFITPSTVPSEINFYNGVLHV 579
++ E ++ HA Q LLG VT+ + D + V + +Y N VLIH+

Sbjct: 92 ATLPDHTPERLIEHAEQMNLLG--VTVEKDTLGDILRLDRDNAVIL-----MTYYRNNVLIHL 145

Query: 580 FIMEAIIAC 588
F + A++AC

Sbjct: 146 FALPALVAC 154

Score = 62 (26.9 bits), Expect = 0.11, Sum P(2) = 0.10

Identities = 22/105 (20%), Positives = 48/105 (45%)

Query: 569 LNFYSNGVLHVFIMEAIIACSLYAVLNKRGLGPGTTPPNLISQQLVKAASLCYLLSN 628
+ +Y N VLIH+F + A++AC N+R IS++ L+R +L L

Sbjct: 135 MTYYRNNVLIHLFALPALVACCFKN--NRR-----ISRDAIIRFVRALYPFLQA 180

Query: 629 EGTISLPCQTFFYQVCHETVGVKFIQYGILTVAEHDDQEDISPSLAE 673
E + + + +F++ G+L A + + + ++ + ++

Sbjct: 181 ELFLRWNEDELNDHIDQWINEFVRQGLLSAGNQEDDTLFRNTSQ 225

16/32

FIG. 4H

View Prodom PD087501

>PD087501 p2001.1 (1) // AIP2-DLD1
 Length = 170

Score = 77 (32.2 bits), Expect = 5.1, P = 0.994
 Identities = 31/114 (27%), Positives = 44/114 (38%)

Query: 51 WKES--LMSRRPFVGRCCYCTPQSNDEKFFNPSISLGLRNVIYINETHTRHRCGLARR 108

W ES L+ RK F RCC F K + L N +H W

Sbjct: 12 WNESEVLVDRKSKFOARCC----PLQXKDIPSILQELTONKNSVSKASHMHMYAWRTAE 67

Query: 109 LSYVLFIQERDVHKGMFATNVTVENLVNLSR--VQ-EAIAEVAELNPDGSAQQ 158

+S L +Q+ KG A + +N SR VQ + I + A+ G+ Q+

Sbjct: 68 VSNLHLQQEQKKKGNKANKSNNSHVNKSRNITVQPKNIEQGCADCGEAGAGQR 121

17/32

FIG. 5A

	10	20	30	40	
1	MDESALT	LG	TIDVSYLPHSSEYSVGRCKHTSEEWGECGFR	56919.pro	
1	MEESSVT	VG	TIDVSYLPSSEYSLGRCKHTSEDWVDCGFK	MouseGPAT.PRO	
1	MEESSVT	IG	TIDVSYLPSSEYSLGRCKHTNEDWVDCGFK	RatGPAT.PRO	
	50	60	70	80	
41	PTVFRS	ATLKW	KESLMSRKRPVGRCCYSCTPQSWDKFFN	56919.pro	
41	PTFFRS	ATLKW	KESLMSRKRPVGRCCYSCTPQSWERFFN	MouseGPAT.PRO	
41	PTFFRS	ATLKW	KESLMSRKRPVGRCCYSCTPQSWERFFN	RatGPAT.PRO	
	90	100	110	120	
81	PSIPSL	GLRN	VIYINETHTRHRGWLARRLSYVLFQERDV	56919.pro	
81	PSIPSL	GLRN	VIYINETHTRHRGWLARRLSYILFVQERDV	MouseGPAT.PRO	
81	PSIPSL	GLRN	VIYINETHTRHRGWLARRLSYILFVQERDV	RatGPAT.PRO	
	130	140	150	160	
121	HKGMF	ATNVT	ENVLNSSRVQEATAEVAAELNPDGSAQQQS	56919.pro	
121	HKGMF	ATSVT	ENVLNSSRVQEATAEVAAELNPDGSAQQQS	MouseGPAT.PRO	
121	HKGMF	ATSIT	DNVLNSSRVQEATAEVAAELNPDGSAQQQS	RatGPAT.PRO	
	170	180	190	200	
161	KAVNK	VKKK	KAKRILOEMVATVSPAMIRLTGWVLLKLFNSF	56919.pro	
161	KAIQK	VKKR	KARKILOEMVATVSPGMIRLTGWVLLKLFNSF	MouseGPAT.PRO	
161	KAIQK	VKKR	KARKILOEMVATVSPGMIRLTGWVLLKLFNSF	RatGPAT.PRO	
	210	220	230	240	
201	FWNIQ	IHKG	QLEMVKAATETNLPILFLPVHRSHIDYLLLT	56919.pro	
201	FWNIQ	IHKG	QLEMVKAATETNLPILFLPVHRSHIDYLLLT	MouseGPAT.PRO	
201	FWNIQ	IHKG	QLEMVKAATETNLPILFLPVHRSHIDYLLLT	RatGPAT.PRO	
	250	260	270	280	
241	FILECH	NIKAP	YIASGNNLNIPFSTLIHKLGFFIRRRRL	56919.pro	
241	FILECH	NIKAP	YIASGNNLNIPVSTLIHKLGFFIRRRRL	MouseGPAT.PRO	
241	FILECH	NIKAP	YIASGNNLNIPFSTLIHKLGFFIRRRRL	RatGPAT.PRO	
	290	300	310	320	
281	DETPD	GRKDV	LYRALLHGHIVELLRQQQFLEIFLEGTRSR	56919.pro	
281	DETPD	GRKD	ILYRALLHGHVVELLRQQQFLEIFLEGTRSR	MouseGPAT.PRO	
281	DETPD	GRKD	ILYRALLHGHIVELLRQQQFLEIFLEGTRSR	RatGPAT.PRO	
	330	340	350	360	
321	SGKT	SCAR	AGLLSVVVDTLSTNVIPDILIPVGISYDRII	56919.pro	
321	SGKT	SCAR	AGVLSVVVNTLSSNTIPDILIPVGISYDRII	MouseGPAT.PRO	
321	SGKT	SCAR	AGLLSVVVDTLSSNTIPDILIPVGISYDRII	RatGPAT.PRO	

18/32

FIG. 5B

	370	380	390	400	
361	EGHYNGEQLGKPKKNESLWSVARGVIRMLRKNYGCVRVDF				56919.pro
361	EGHYNGEQLGKPKKNESLWSVARGVIRMLRKNYGYVRVDF				MouseGPAT.PRO
361	EGHYNGEQLGKPKKNESLWSVARGVIRMLRKNYGYVRVDF				RatGPAT.PRO
	410	420	430	440	
401	AQPFSLKEYLESQSQKPVSAIISLEQALLPAILPSRPSDA				56919.pro
401	AQPFSLKEYLEGQSQKPVSAIISLEQALLPAILPSRPNDV				MouseGPAT.PRO
401	AQPFSLKEYLEGQSQKPVSAIISLEQALLPAILPSRPDAA				RatGPAT.PRO
	450	460	470	480	
441	ADEGRDTSINESRNATDESLRRRLIANLAEHILFTASKSC				56919.pro
441	ADEHQDLSINESRNPADEAFRRRLIANLAEHILFTASKSC				MouseGPAT.PRO
441	AAEHEDMSINESRNAADEAFRRRLIANLAEHILFTASKSC				RatGPAT.PRO
	490	500	510	520	
481	AIMSTHIVACLLLYRHRQGIIDLSTLVEDFFVMKEEV LARD				56919.pro
481	AIMSTHIVACLLLYRHRQGIHLSTLVEDFFVMKEEV LARD				MouseGPAT.PRO
481	AIMSTHIVACLLLYRHRQGIHLSTLVEDFFVMKEEV LARD				RatGPAT.PRO
	530	540	550	560	
521	FDLGFSGNSEDVVMHAIQLLGNCVTITHTSRNDEFFITPS				56919.pro
521	FDLGFSGNSEDVVMHAIQLLGNCVTITHTSRKDEFFITPS				MouseGPAT.PRO
521	FDLGFSGNSEDVVMHAIQLLGNCVTITHTSRKDEFFITPS				RatGPAT.PRO
	570	580	590	600	
561	TTVPSVFELNFYSNGVLHVFIMEAIIACSLYAVLNKRGLG				56919.pro
561	TTVPSVFELNFYSNGVLHVFIMEAIIACSLYAVLNKRCSG				MouseGPAT.PRO
561	TTVPSVFELNFYSNGVLHVFIMEAIIACSLYAVQNKRGS				RatGPAT.PRO
	610	620	630	640	
601	GPTSTPPNLISQEQLVRKAASLCYLLSNEG TISLPCQTFY				56919.pro
601	GPTSTPPNLISQEQLVRKAASLCYLLSNEG TISLPCQTFY				MouseGPAT.PRO
601	GPTSTPPNLISQEQLVRKAASLCYLLSNEG TISLPCQTFY				RatGPAT.PRO
	650	660	670	680	
641	QVCHETVGKFIQYGILTVAEHDDQEDISPSLAEQQWDKKL				56919.pro
641	QVCHETVGKFIQYGILTVAEQDDQEDVSPGLAEQQWDKKL				MouseGPAT.PRO
641	QVCQETVGKFIQYGILTVAEQDDQEDVSPGLAEQQWNKKL				RatGPAT.PRO
	690	700	710	720	
681	PEPLSWRSDEEDEDSDFGEEQRDCYLKVSQSKEHQOFITF				56919.pro
681	PE-LNWSRSDEEDEDSDFGEEQRDCYLKVSQSKEHQOFITF				MouseGPAT.PRO
681	PEPLNWSRSDEEDEDSDFGEEQRDCYLKVSQAKEHQOFITF				RatGPAT.PRO

19/32

FIG. 5C

	730	740	750	760	
721	LQRLG	PLLEAYSSAAIFVHN	FSGPVPEPEY	LQKLHKYLI	56919.pro
721	LQRLG	PLLEAYSSAAIFVHN	FSGPVPEPEY	LQRLHKYLI	MouseGPAT.PRO
721	LQRLG	PLLEAYSSAAIFVHT	FRGPVPEPEY	LQRLHKYLI	RatGPAT.PRO
	770	780	790	800	
761	TRTERNVAVYAESATY	CLVKN	AVKMFKD	IGVFKETKQKRV	56919.pro
761	TRTERNVAVYAESATY	CLVKN	AVKMFKD	IGVFKETKQKRV	MouseGPAT.PRO
761	TRTERNVAVYAESATY	CLVKN	AVKMFKD	IGVFKETKQKRA	RatGPAT.PRO
	810	820			
801	SVLELSSTFLPQCN	RQKLLEYILSFVVL			56919.pro
801	SVLELSSTFLPQCN	RQKLLEYILSFVVL			MouseGPAT.PRO
801	SVLELSSTFLPQCN	RQKLLEYILSFVVL			RatGPAT.PRO

20/32

FIG.6

Acyltransferase catalytic motif-I

<u>IFLEGTRSR</u>	56919.pro
IFLEGTRSR	MouseGPAT.PRO
IFLEGTRSR	RatGPAT.PRO
YFVEGGRSR	EcoliGPAT.PRO

Acyltransferase catalytic motif-II

<u>HRSHID</u>	56919.pro
HRSHID	MouseGPAT.PRO
HRSHID	RatGPAT.PRO
HRSHMD	EcoliGPAT.PRO

Acyltransferase catalytic motif-III

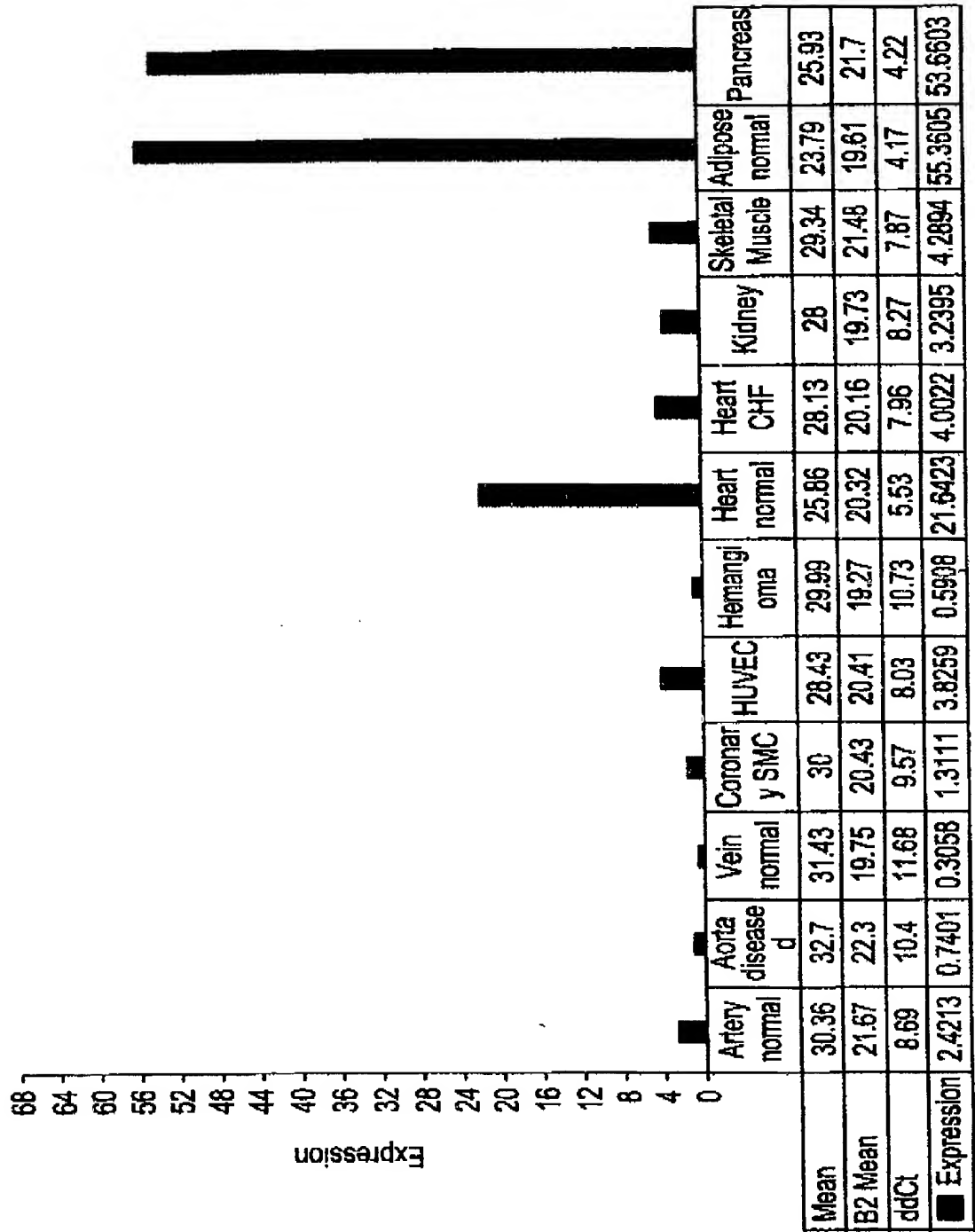
<u>ILIIPV</u>	56919.pro
ILVIPV	MouseGPAT.PRO
ILVIPV	RatGPAT.PRO
ITLIPI	EcoliGPAT.PRO

Acyltransferase signature motif

<u>GGFFIRR</u>	56919.pro
GGFFIRR	MouseGPAT.PRO
GGFFIRR	RatGPAT.PRO
GAFFIRR	EcoliGPAT.PRO

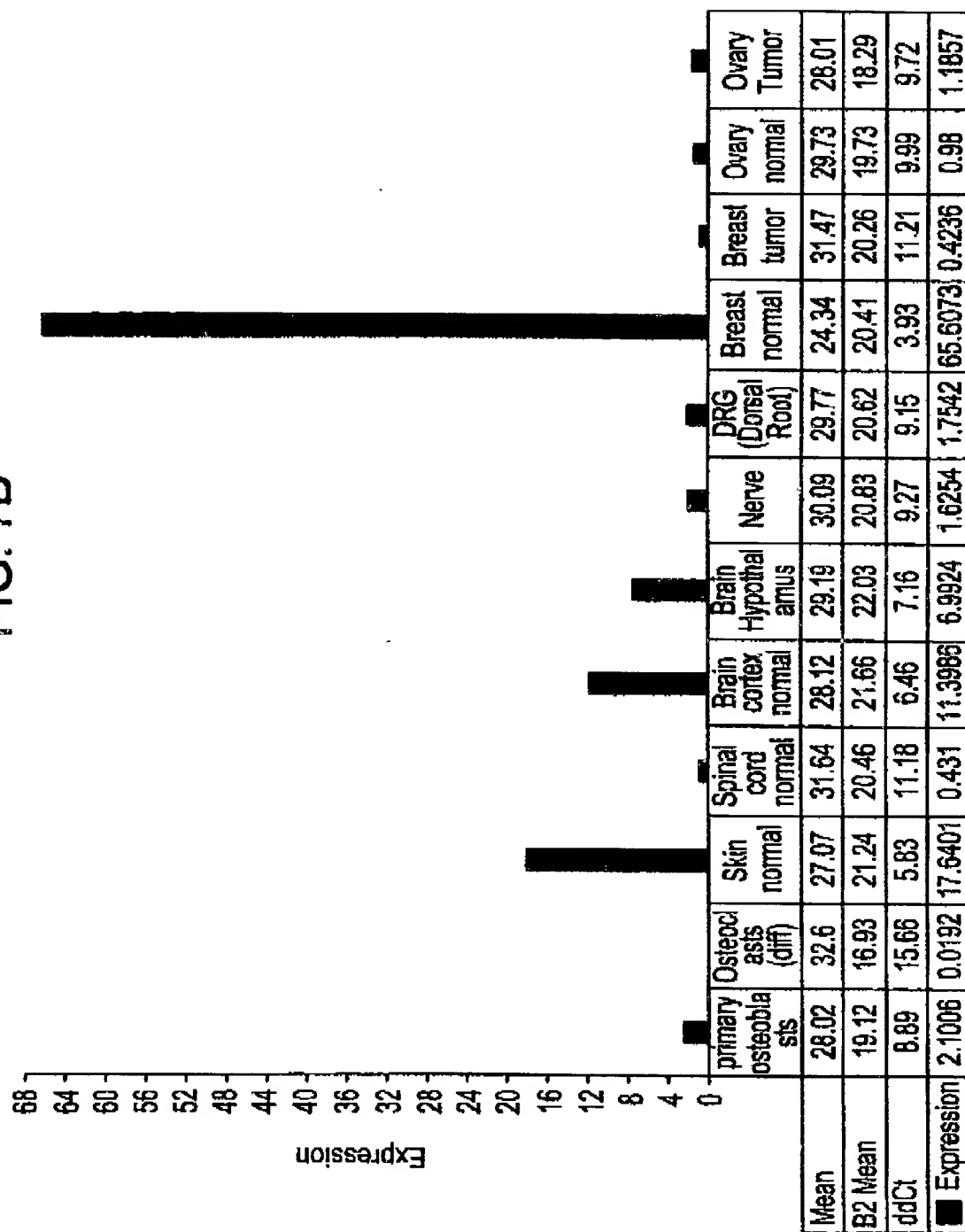
21/32

FIG. 7A



22/32

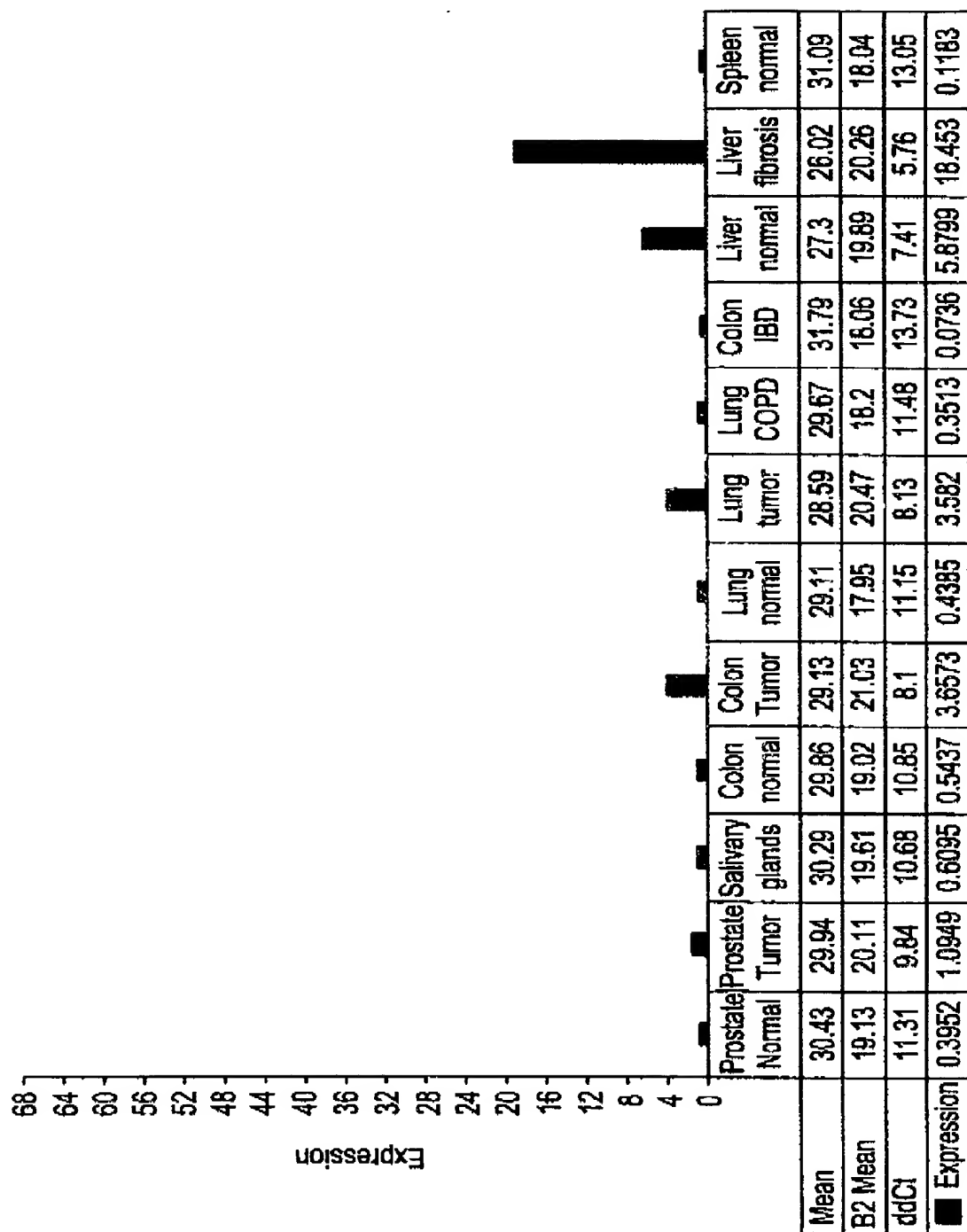
FIG. 7B



09935290.030402

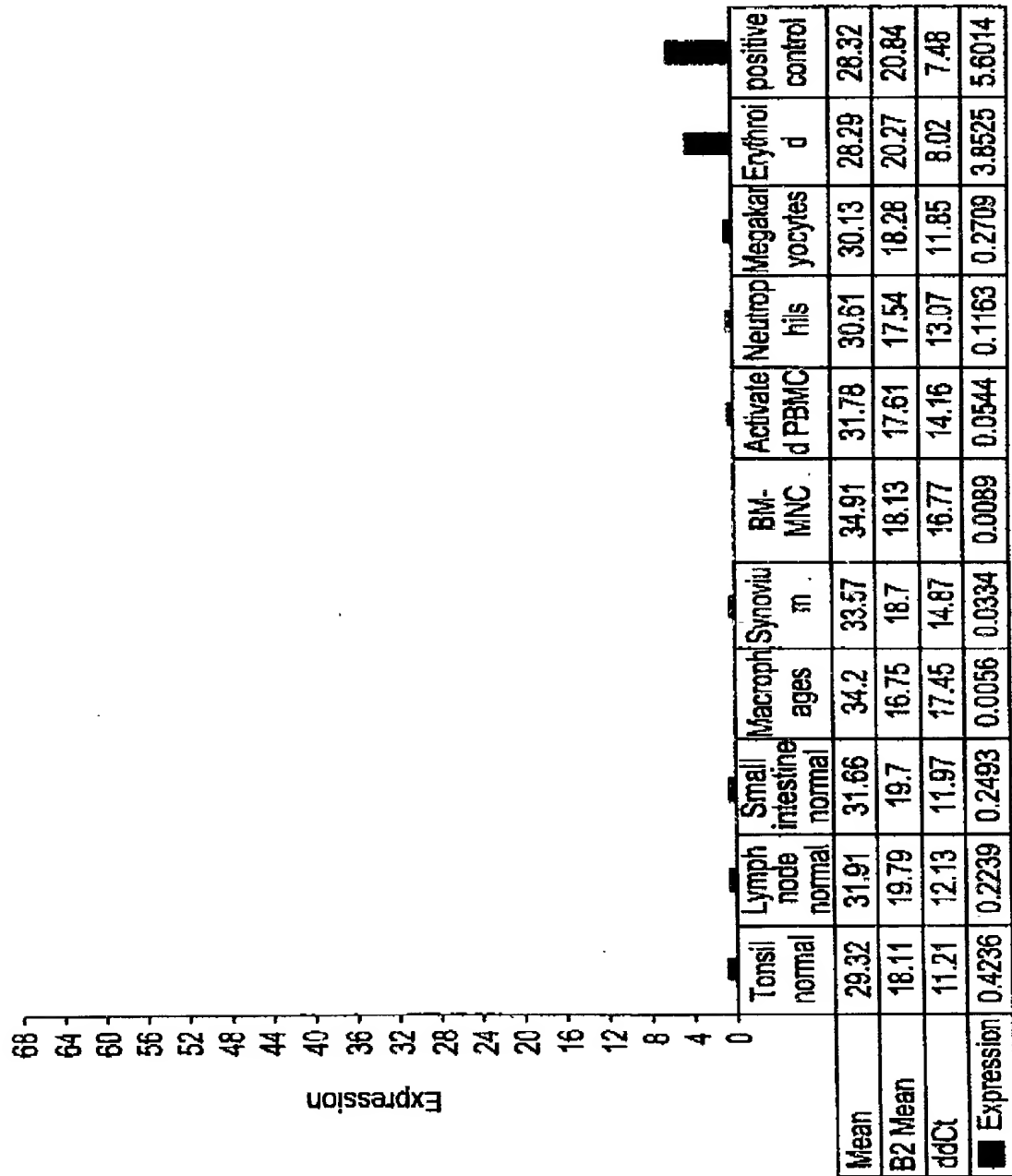
23/32

FIG. 7C



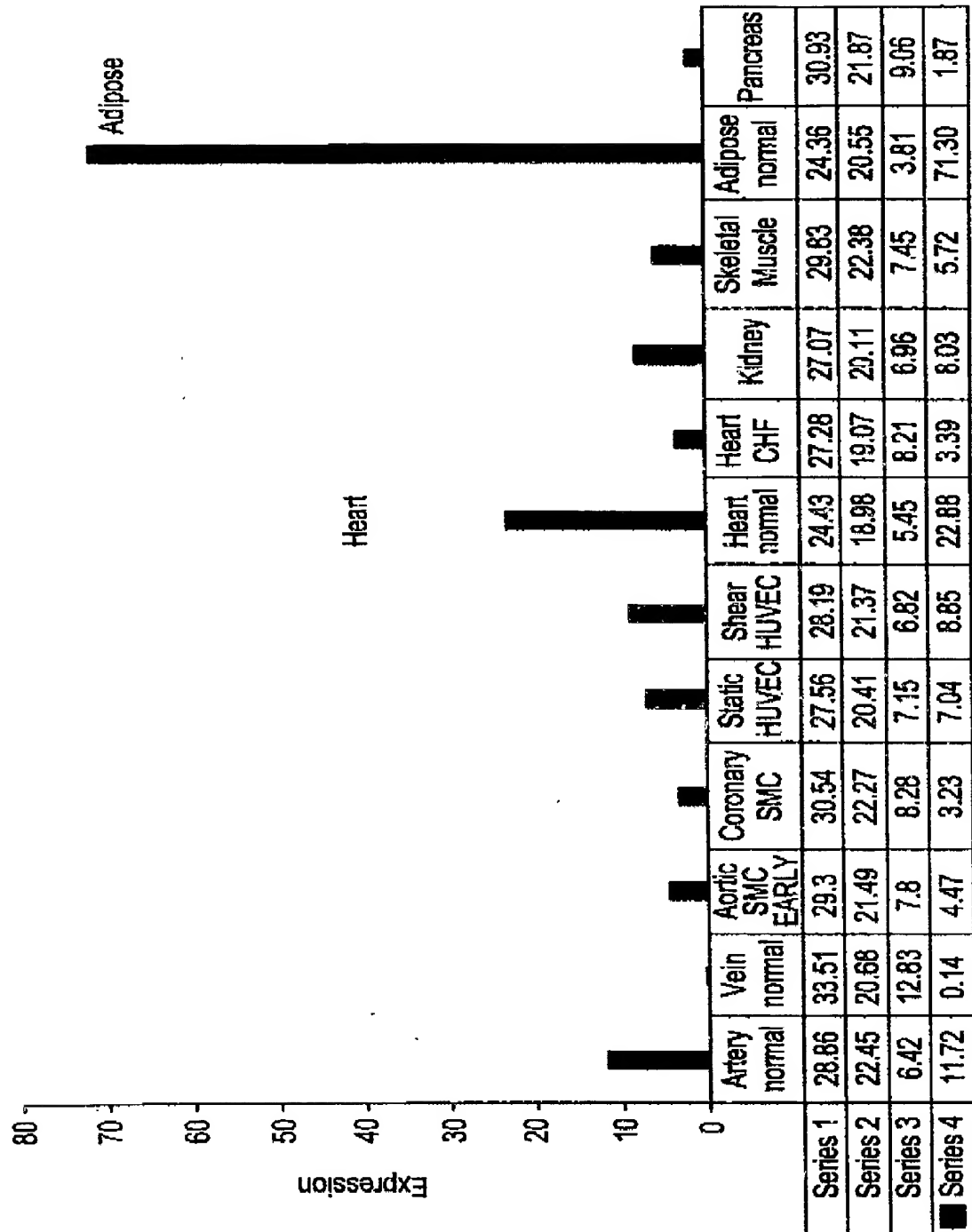
24/32

FIG. 7D



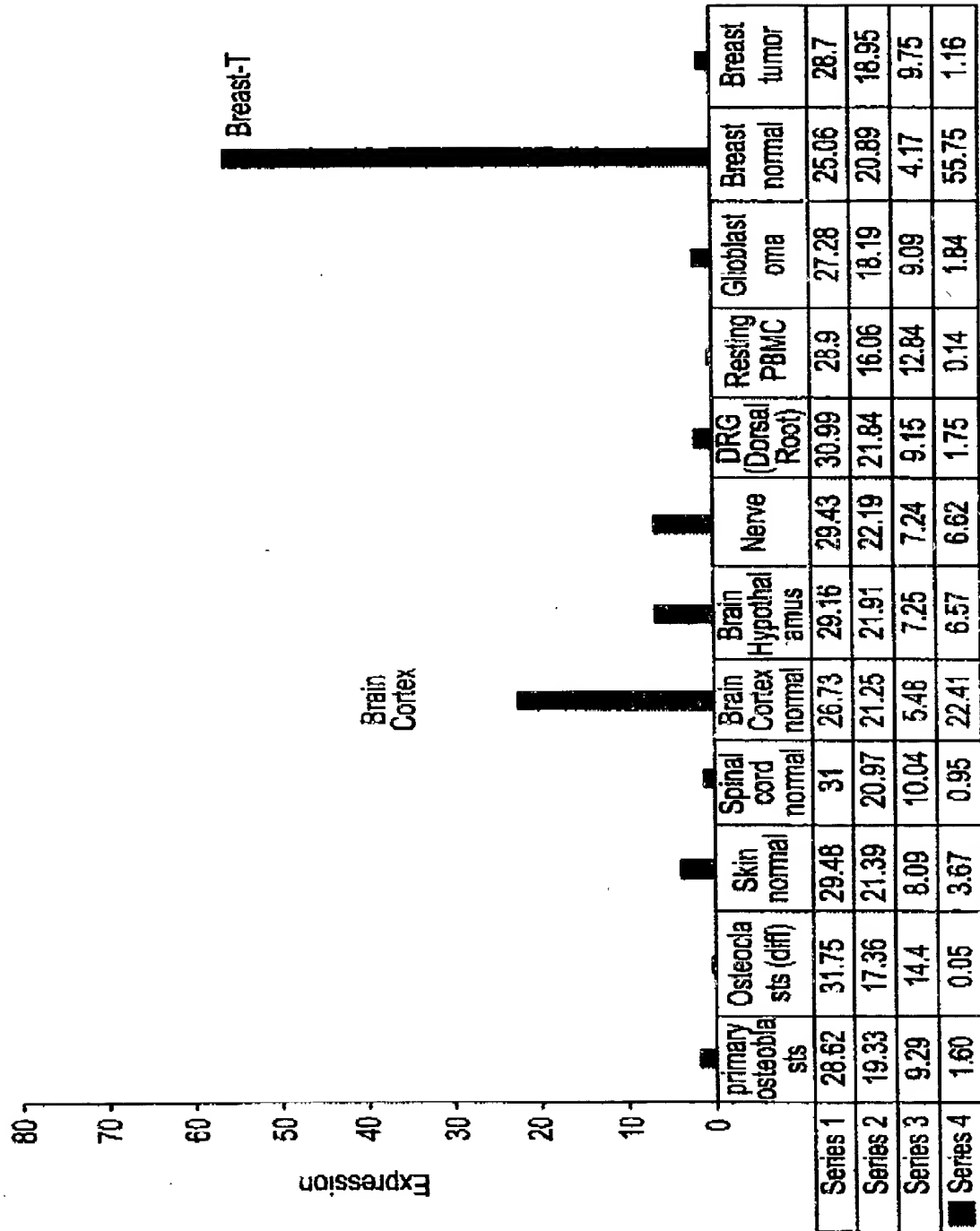
25/32

FIG. 8A



26/32

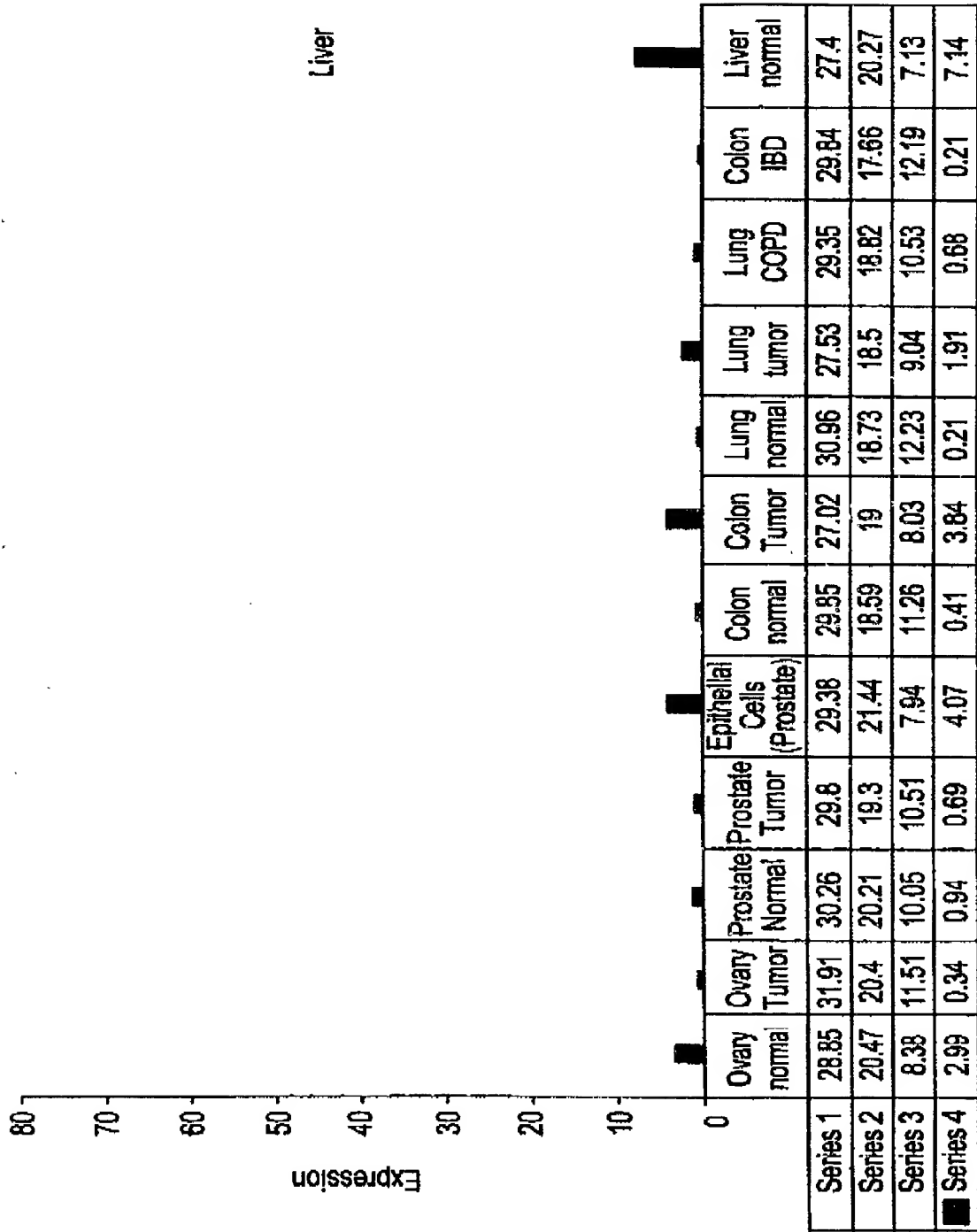
FIG. 8B



27/32

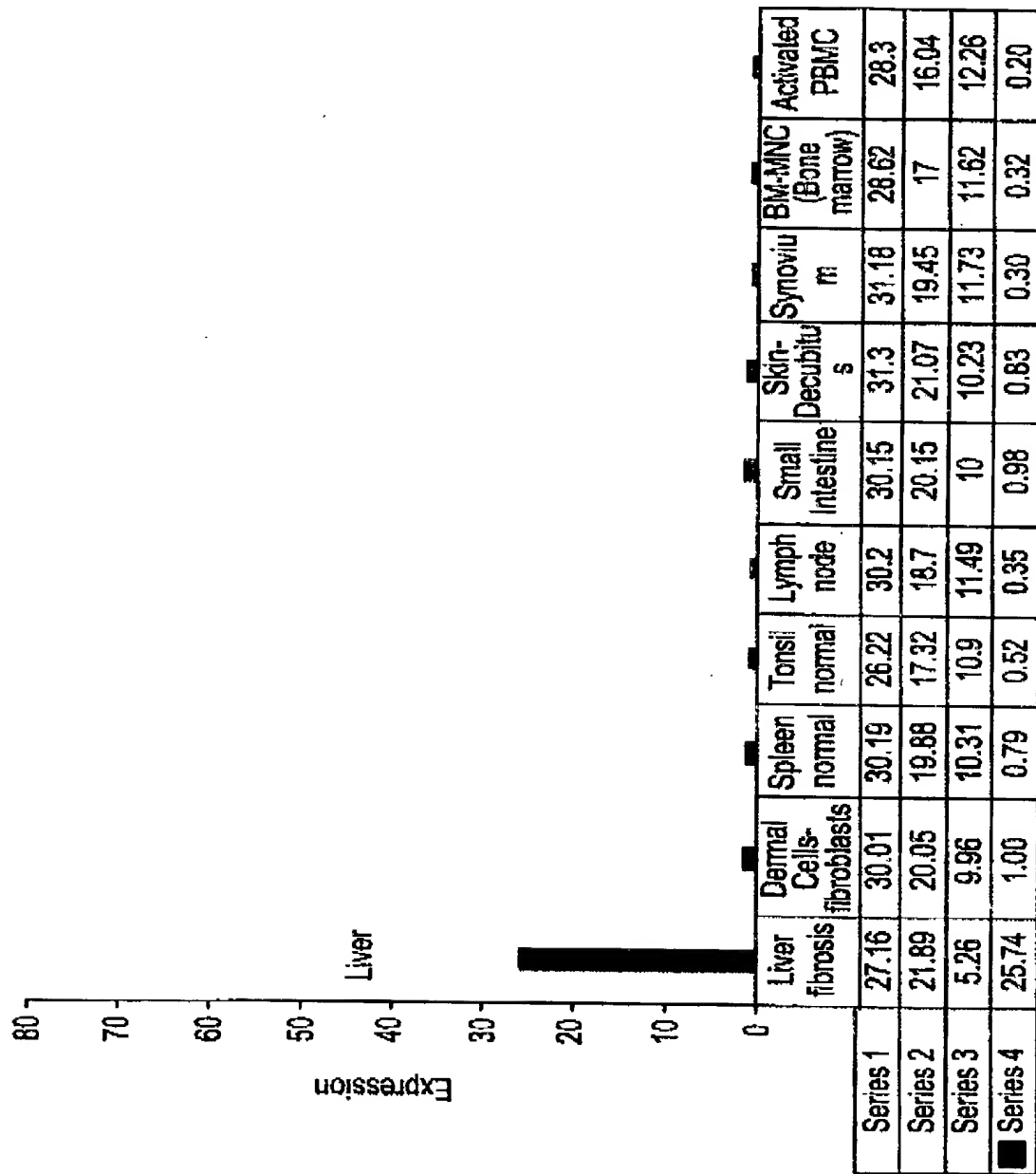
Liver

FIG. 8C



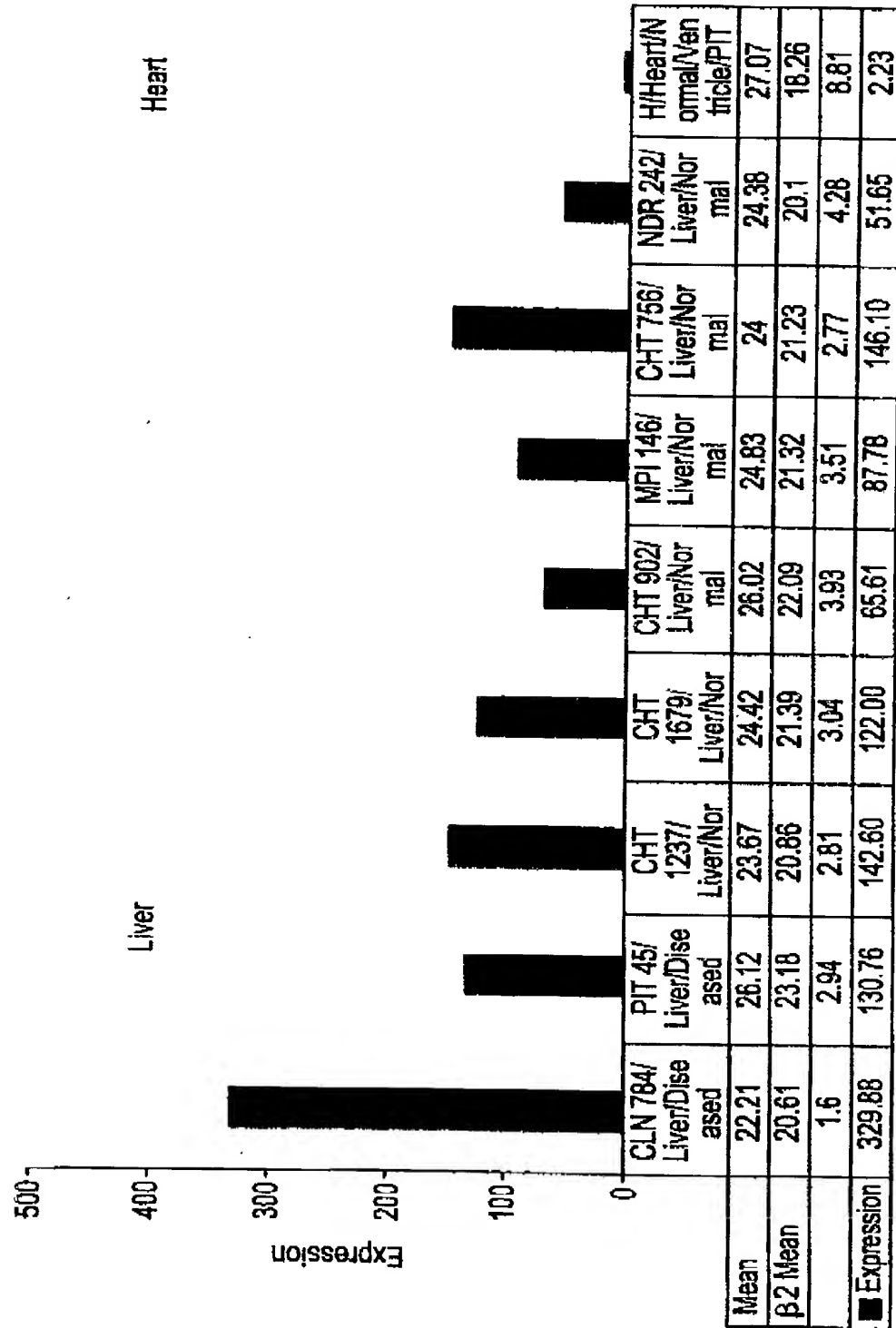
28/32

FIG. 8D



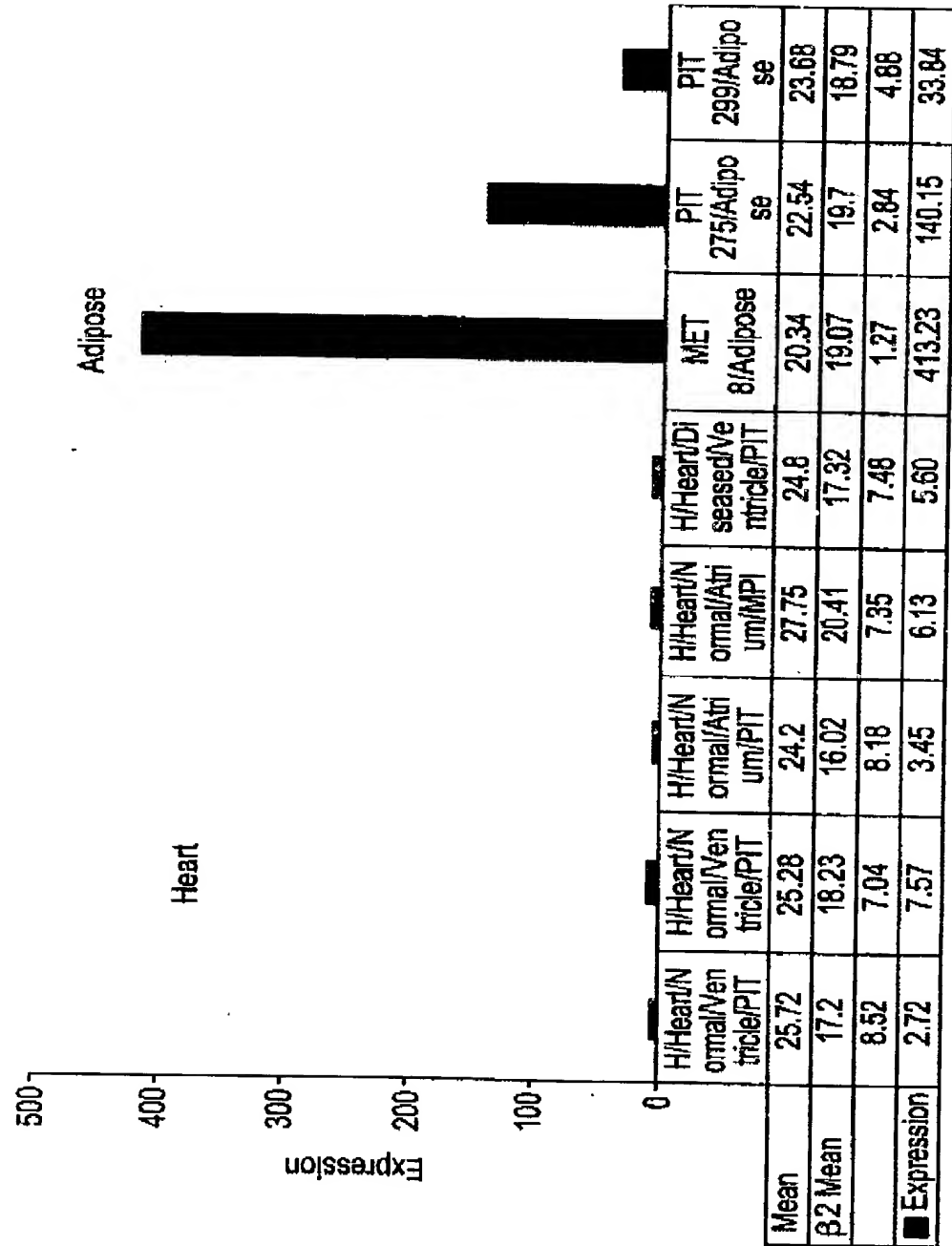
29/32

FIG. 9A



30/32

FIG. 9B



32/32

FIG. 10B

